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IMPROVING CLINICALLY RELEVANT BACTERIAL SPECIES IDENTIFICATION: A COMPUTATIONAL APPROACH USING KONSTANZ INFORMATION MINER (KNIME) PLATFORM

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Determining clinically important bacterial species remains a significant challenge for clinical microbiology laboratories with limited access to advanced diagnostic tools, where delays or misidentifications can compromise patient outcomes and contribute to inappropriate antibiotic use. The purpose of this research was to create a computational system through KNIME that enhanced bacterial species determination by integrating CLSI standard procedures with protocols from Cowan and Steel's Manual. The research value stems from offering a cost-friendly diagnostic enhancement strategy which improves efficiency throughout regular microbiology testing facilities. This research aimed to conduct a systematic analysis of existing identification problems, develop and optimise computational models, evaluate diagnostic effectiveness and resource needs, and validate model performance using hospital-recorded datasets. In this research, two workflows were designed on KNIME. The broad-spectrum workflow was designed to identify 445 species, encompassing rare, common, and less common species. The narrow-spectrum workflow focused on identifying 145 species, primarily common and less common species. The workflow's user interface was developed to enable user-friendly interaction with the KNIME based bacterial identification system. The system interface allows users to input clinical information such as sample type, gram stain results, culture characteristics, and biochemical test results. The system processes these inputs and generates the most possible bacteria species and antibiotics as output. System validation occurred through testing 200 clinical specimens derived from the Teaching Hospital, Peradeniya. The bacterial identification model reached outstanding performance levels with 99.8% accuracy and 98.5% recall, but 94.6% precision and 99.3% specificity alongside an F1 score of 96.5%. The antibiotic selection component performed at a moderate accuracy of 78.0%. Testing confirmed the reliability of the developed computational workflow, which provided bacterial identification services alongside antibiotic selection capabilities. The research demonstrates how combining traditional microbiological procedures with computational systems creates improved diagnostic pipelines to enhance clinical diagnosis while benefiting resource-constrained healthcare settings.

Keywords: Bacterial species identification, Clinical microbiology**,** Computational workflow**,** Diagnostic efficiency, KNIME